

1/16

Figure 1

IM2169

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M978

```

      10      20      30      40      50      60
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSEKPAQKDQGGYGFMRLKRRNWYPGAE--ESEVKLNESDW
=====
CLGGGGTDFDLSVDTEAPRPAPKYQDVSSEKPAQKDQGGYGFMRLKRRNWHFQANPKEDIKSENDW
      10      20      30      40      50      60      70

      70      80      90     100     110     120     130
EATGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLTPSNHQNGSAGNGVNPKNQATGHENFQYVYSG
=====
EATGLPGNPKNLPERQKSVIEKVKTGSDSNIYSSPYLTQSNHQNGSA-N---QPKNEVKDYKEFKYVYSG
      80      90     100     110     120     130

      150     160     170     180     190     200
WFKYKHAASE--KDFS-NKKIKSGDDGYIFYHGEKPSRQLPASGKVYKGVWHFVTDTKKGQDFREIIQPS
=====
WFKYKHALEIIKENNLKGAKSDDGYIFYHGEKPSRQLPVSGEVYKGVWHFVTDTKQGQKFNDILGTS
      140     150     160     170     180     190     200

      210     220     230     240     250     260     270
KKQGDYSGFSGDGSEEYSNKNESTLKDDHEGYGFTSNLEVDGNNKKLTGKLI RNNASLNNNTNNDKHTT
=====
KKQGDYSGFPGDDGEEYSNKNEATLQGSQEGYGFTSNLKVDNFNKKLTGELIRNN-RVTNATANDKYTT
      210     220     230     240     250     260     270

      280     290     300     310     320     330     340
QYYSLEAQITGNRFNGTATATDKKEN-ETKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVGSA
=====
QYYSLEAQVTGNRFNGKATATDKPGTGETKQHPFVSDSSSLSGGFFGPKEELGFRFLSNDQKVAVVGSA
      280     290     300     310     320     330     340

      350     360     370     380     390     400     410
KTKDKLENG--AAASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIM
=====
KTQDKAANGNTAAASGGTDAAASNGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIM
      350     360     370     380     390     400     410

      420     430     440     450     460     470
IPLLPKDSESGNTQADKKGK---NG--G-TEFTRKFEHTPESDKKD--AQAGTQ-TNGAQTASNTAGDTNG
=====
IPLLPESESQADKKGKNGKNGGTDFTYKTTYTPKNDDKDTKAQTGAAGSSGAQTDLGKADVNGG
      420     430     440     450     460     470     480

      480     490     500     510     520     530     540
K--TKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQN
=====
KAETKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPNDQN
      490     500     510     520     530     540     550
```

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550 560 570 580 590 600 610
VVYRGSWYGHIANGTWSGNASDKEGGNRAEFTVNFADKKITGKLTAE NRQAQTFTIEGMIQGN GFEGTA
=====

560 570 580 590 600 610 620
VVYRGSWYGHIASSTWSGNASNATSGNRAEFTVNFDTKKINGTLTAENRQEATFTIDGKIEGN GFSGTA
=====

620 630 640 650 660 670 680
KTAESGFDLDQKNTRTPKAYITDAKVGGFYGPKAELGGWFAYPGDKQTEKATATSSDGN SASSATVV
=====

630 640 650 660 670 680 690
KTADLGFDLDQSNTTGTTPKAYITDAKVGGFYGPKAELGGWFAYPGDKQTEKATVASGDGN SASSATVV
=====

690
FGAKRQQPVQ
=====

700
FGAKRQQPVQ

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Figure 2

IM2169

6940

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      10      20      30      40      50      60      70
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSEKPAQKQDGGYGFAMRLKRRNWYPGAESEVKLNESDWEA
=====
CLGGGGTFDLDSVDTEAPRPDPKYQDVSSEKPAQKQDGGYGFAMRLKRRNWYSAAKEDEVKLNESDWET
      10      20      30      40      50      60      70

      80      90     100     110     120     130
TGLPTKPKELPKRQKSVIEKVETD-GDSDIYSSPYLTPSNHQNGSAGNGVNQPKNQATGHENFQYVYSGW
=====
TGLPTEPKKLPLKQESVISKVQANNGDNNIYTSPLYLTQSNHQNSSINGGANLPKNEVTNYKDFKYVYSGW
      80      90     100     110     120     130     140

      150     160     170     180     190     200
FYKHAASE--KDFSNNK-IKSGDDGYIFYHGKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQPSK
=====
FYKHAKNEIIRENSSIKGAKNGDDGYIFYHGKPSRQLPASGTVTYKGVWHFATDVKKSONFRDIIQPSK
      150     160     170     180     190     200     210

      210     220     230     240     250     260     270
KQGDYSGFSGDGGSEESYNNKNESTLKDDHEGYGFTSNLEVDFGNKKLTGKLI RNNASLNNNTNNDKHTTQ
=====
KQGDYSGFSGDDDEQYSNNKNESTLKDDHEGYGFTSNLEVDFGSKKLTGKLI RN--RVTNAPTNDKYTTQ
      220     230     240     250     260     270

      280     290     300     310     320     330     340
YYSLDAQITGNRFRNGTATATDKKENE-TKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVGS AK
=====
YYSLDAQITGNRFRNGKAIRTDKPD TGKTLHPFVSDSSSLSGGFFGPKEELGFRFLSDDKKVAVVGS AK
      290     300     310     320     330     340

      350     360     370     380     390     400     410
TKDKLENGAAASGSTGAAASGGAAGTSSSENSKLT TVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIM I PL
=====
TKDKTENGAVASGGTDAAASNGAAGTSSSENSKLT TVLDAVELKLGDKEVQKLDNFSNAAQLVVDGIM I PL
      360     370     380     390     400     410

      420     430     440     450     460     470     480
LPKDESNGTQADKGKNGGTEFTTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCS
=====
LPEASESGNNQANQGTNGGTAFTTRKFDHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCS
      430     440     450     460     470     480

      490     500     510     520     530     540     550
NLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQNVVYRGSWYGH I ANG
=====
NLNYLKYGMLTRKNSKSAMQAGSSSQADAKTEQVEQSMFLQGERTDEKEIPSEQNIVYRGSWYGY I ANG
      500     510     520     530     540     550

      560     570     580     590     600     610     620
--TSWSGNASDKEGGNRAEFTVNFADKKITGKLTAE NRQAQTFTIEGMIQGNGFEGTAKTAESGF DLDQK
=====
KSTWSGNASNATSGNRAEFTVNFADKKITGTLTADNRQEATFTIDGNIKDN GFEGTAKTAESGF DLDQS
      570     580     590     600     610     620
```

630	640	650	660	670	680	690
NTTTRTPKAYITDAKVKGFFYGPKAEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQQPVQ						
=====						
NTTTRTPKAYITDAKVQGGFYGPKEELGGWFAYPGDKQT-KN-ATNASGNS-S-ATVVFGAKRQQPVR						
640	650	660	670	680	690	

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Figure 3

IM2169

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S3032

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      10      20      30      40      50      60
CLGGGG-SFDLDSVDTEAPRPAPKYQDVSSEKPAQKQDQGGYGAMRLKRRNWYPGAEESEVKLNESDWE
=====
CLGGGGGSFDLDSVDTEAPRPAPKYQDVSSEKPAQKQDQGGYGAMRLKRRNWYPSAKENEVKLNESDWE
      10      20      30      40      50      60      70

      80      90     100     110     120     130
ATGLPTKPKELPKRQKSVEIKVETDGDSD---IYSSPYLTFSNHQNGSAGNGVNQPKNQATGHENFQYVY
-----
TTGLPSNPKNLPERQKSVIDQVETDGDSSNNSNIYSSPYLTQSNHONGNTGNGVNQPKNEVTDYKNFKYVY
      80      90     100     110     120     130     140

      140     150     160     170     180     190     200
SGWIFYKHAASEKDFS-NKKI-KSGDDGYIFYHGEKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQP
=====
SGWIFYKHAKREVNLAPEPKIAKNGDDGYIFYHKGDPQRQLPASGKITIKGVWHFATDTKRGQKFREIIQP
      150     160     170     180     190     200     210

      210     220     230     240     250     260     270
SKKQGDRIYSGFSGDGSEEYSNKNESLTKDDHEGYGFTSNLEVDGNGKLTGKLI RNNASLNNNTNNDKHT
==
SKNQGDRIYSGFSGDDDEQYSNKNESMLKDGHEGYGFASNLEVDGDNKLTGKLI RNNANQNNTNNDKHT
      220     230     240     250     260     270     280

      280     290     300     310     320     330     340
TQYYSLDAQITGNRFNGTATATDK-KEN-ETKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVG
=====
TQYYSLDATLKGNRFSGKAEATDKPKNDGETKEHPFVSDSSSLSGGFFGPQGEELGFRFLSNDQKVAVVG
      290     300     310     320     330     340     350

      350     360     370     380     390     400     410
SAKTKDKLENG-AA-ASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDG
=====
SAKTKDKPANGNTAEASGGTDAAASGGAAGTSSSENSKLTTVLDAVELTHGGTAIKNLDNFSNAAQLVVDG
      360     370     380     390     400     410     420

      420     430     440     450     460     470     480
IMIPLLPKDSESGNTQADKGKNGGTEFTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEV
=====
IMIPLLQNSTGKNNQPDQKGKNGGTAFIYKTTYTPKNDDKDTKAQTVTGGTQTASNTAGDANGKTKTYEV
      430     440     450     460     470     480     490

      490     500     510     520     530     540     550
EVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLOGERTDEKEIPTDQNVVYRGSWYG
=====
EVCCSNLNYLKYGLLTRKTAGNTVGSGNSSPTAAQTDAA--QSMFLOGERTDENKIPSEQNVVYRGSWYG
      500     510     520     530     540     550

      560     570     580     590     600     610     620
HIANGTSWGSNASDKEGGNRAEFTVNFADKKITGKLTAEENRQAQFTTIEGMIQGNNGFEGTAKTAESGFDL
=====
HIASSTSWGSNASDKEGGNRAEFTVNFGEKKITGTLTAENRQEAFTTIDGKIEGNGFGSGTAKTAELGFDL
      570     580     590     600     610     620
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630	640	650	660	670	680	690
DQKNTTRTPKAYITDAKVKGGFYGPKAEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQOPVQ						
=====						
DQKNTTRTPKAYITDAKVKGGFYGPKAEELGGWFAYSDDKQTKNATDASGNGNSASSATVVFGAKRQOPVQ						
640	650	660	670	680	690	

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Figure 4

	10	20	30	40	50	60	
346		361		380			
1	TKDKLENGAA--ASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						58
2	TKDKTENGAV--ASGGTDAAASNGAAGTSSSENSKLTTVLDAVELKLGDKEVQKLDNFSNA						58
3	TKDKTENGAV--ASGGTDAAASNGAAGTSSSENSKLTTVLDAVELKLGDKEVQKLDNFSNA						58
4	TQDKPRNGAV--ASGGTGAARSNGAAGQSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						58
5	TQDKAANGNTAAASGGTDAAASNGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						60
6	KRDKAESGGGNGASGGTDAAASNGAAGTSSSENSKLTTVLDAVELKSGGKEVKNLDNFSNA						60
7	TKDKPRNGAV--ASGGTDAAASNGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						58
8	TKDKPANGNTAEASGGTDAAASGGAAGTSSSENSKLTTVLDAVELTHGGTAIKNLDNFSNA						60
9	TKDKPGNGA---RLQAARCGTSNGAAGQSSSENSKLTTVLDAVELKLGDKEVQKLDNFSNA						57
C	*+DK::*G+:+:*****+*+S+GAAG+SSEN*KLTTVLDAVEL:++*+:++LDNFSNA						

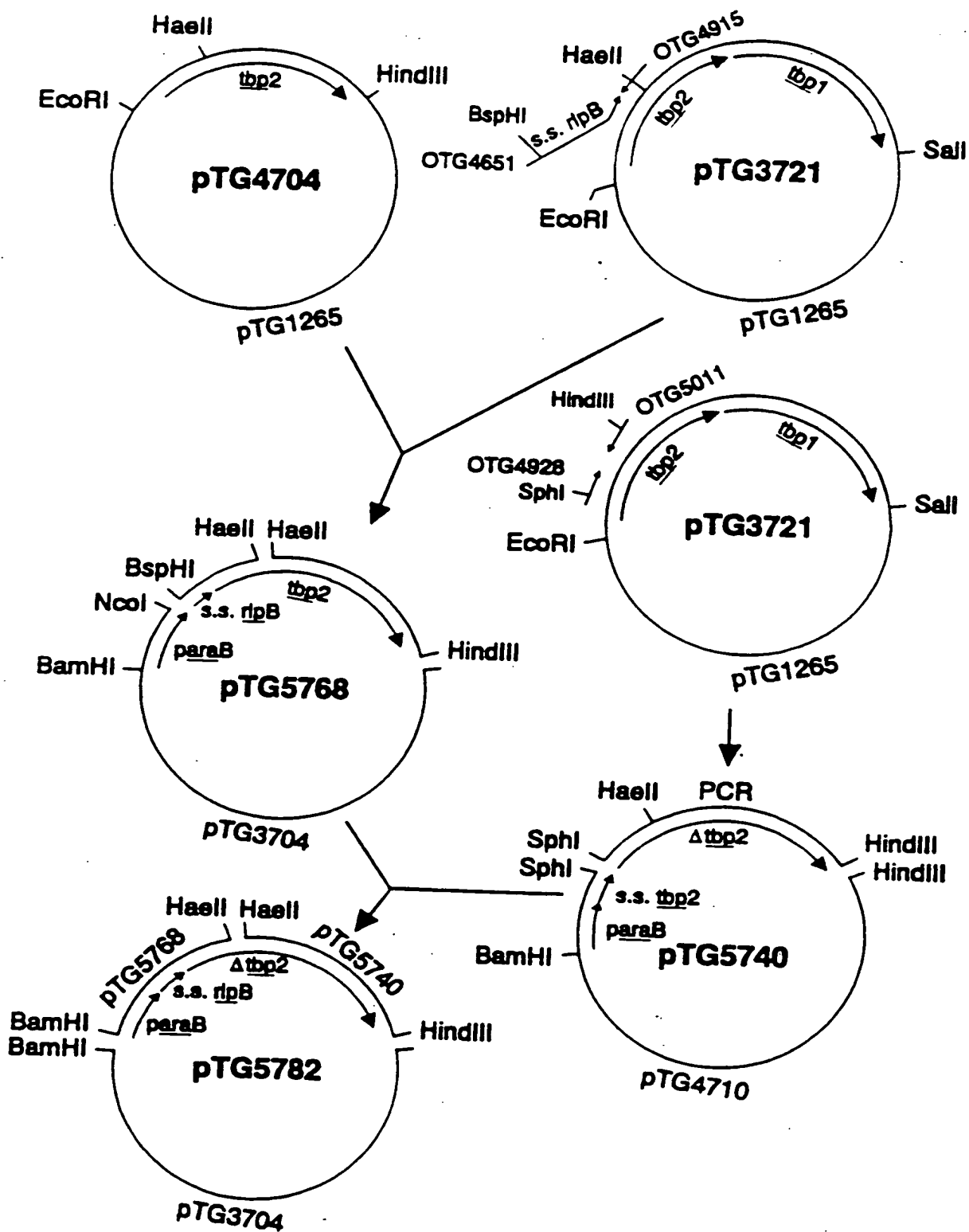
	70	80	90	100	110	120	
	417				445		
1	AQLVVDGIMIPLLPKDSESGNTQADK GK-----NGGTEFTRKFEHTPESDKKDAQAGTQ						112
2	AQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTTRKFDHTPESDKKDAQAGTQ						112
3	AQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTTRKFDHTPESDKKDAQAGTQ						112
4	AQLVVDGIMIPLLPEASESGKNQANQGT-----NGGTAFTTRKFNETPKSDEKDTQAGTA						112
5	AQLVVDGIMIPLLPETSESGSNQADK GKKGNGKNGGTDFTYKTTYTPKNDDKDTKAQTG						120
6	AQLVVDGIMIPLLPKDSESGNTQADK GK-----NGGTFTRKFEHTPESDKKDAQAGTQ						114
7	AQLVVDGIMIPLMPETSESGNNQADK GK-----NGGTAFTTRKFDHTPKSDEKDTQAGTP						112
8	AQLVVDGIMIPLLQNSTGKNNQPDQ GK-----NGGTAFTYKTTYTPKNDDKDTKAQTV						114
9	AQLVVDGIMIPLLPKDSESGKNQADK GK-----NGETEFTTRKFEHTPESDEKDAQAGTP						111
C	AQLVV*GIMIPL*P:.S***+*Q*+:G: NG*T:F*+K*+.TP:+D:KD:+A+T:						

	130	140	150	160	170	180	
	465		482		499		
1	TNGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGGNSSQ						167
2	TNGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGESSQ						167
3	ANGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGESSQ						167
4	ENGNPAASNTAGDANGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGESSQ						167
5	AAGSSGAQTDLGKADVNGGKRAETKTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGGNSSQ						180
6	TNGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGLLTRKTAGNTGEGGNGSQT						169
7	TNGAQTASGTAGVTGGQAG-----KTYAVEVCCSNLNYLKYGLLTRKTADNTVGSGNGSSST						168
8	TGGTQTASNTAGDANGKT-----KTYEVEVCCSNLNYLKYGLLTRKTAGNTVGSGNGSSPT						169
9	SNGAQTASNTAGDTNGKT-----KTYEVNLC-SNLNYLKYGLLTRKTAGNTGEGGNGSSPT						165
C	:+G+++A***G+++++. KTY*V**C*SNLNYLKYG:LTRK:::G::S+:						

	190	200	210	
	521			
1	ADAKTEQVEQSMFLQGERTDEKEIPTDQ-NVV			198
2	ADAKTEQVEQSMFLQGERTDEKEIPSEQ-NIV			198
3	ADAKTEQVGQSMFLQGERTDEKEIPSEQ-NIV			198
4	ADAKTEQVGQSMFLQGERTDEKEIPNDQ-NVV			198
5	ADAKTEQVEQSMFLQGERTDEKEIPNDQ-NVV			211
6	AAAQTAQGAQSMFLQGERTDEKEIPSEQ-NVV			200
7	AAAQTAQGAQSMFLQGERTDEKEIPKEQQDIV			200
8	AAAQTD--AQSMFLQGERTDENKIPSEQ-NVV			198
9	AA-QTAQGAQSMFLQGERTDEKEIPNDQ-NVV			195
C	A:::T:::QSMFLQGERTDE**IP::Q *+V			

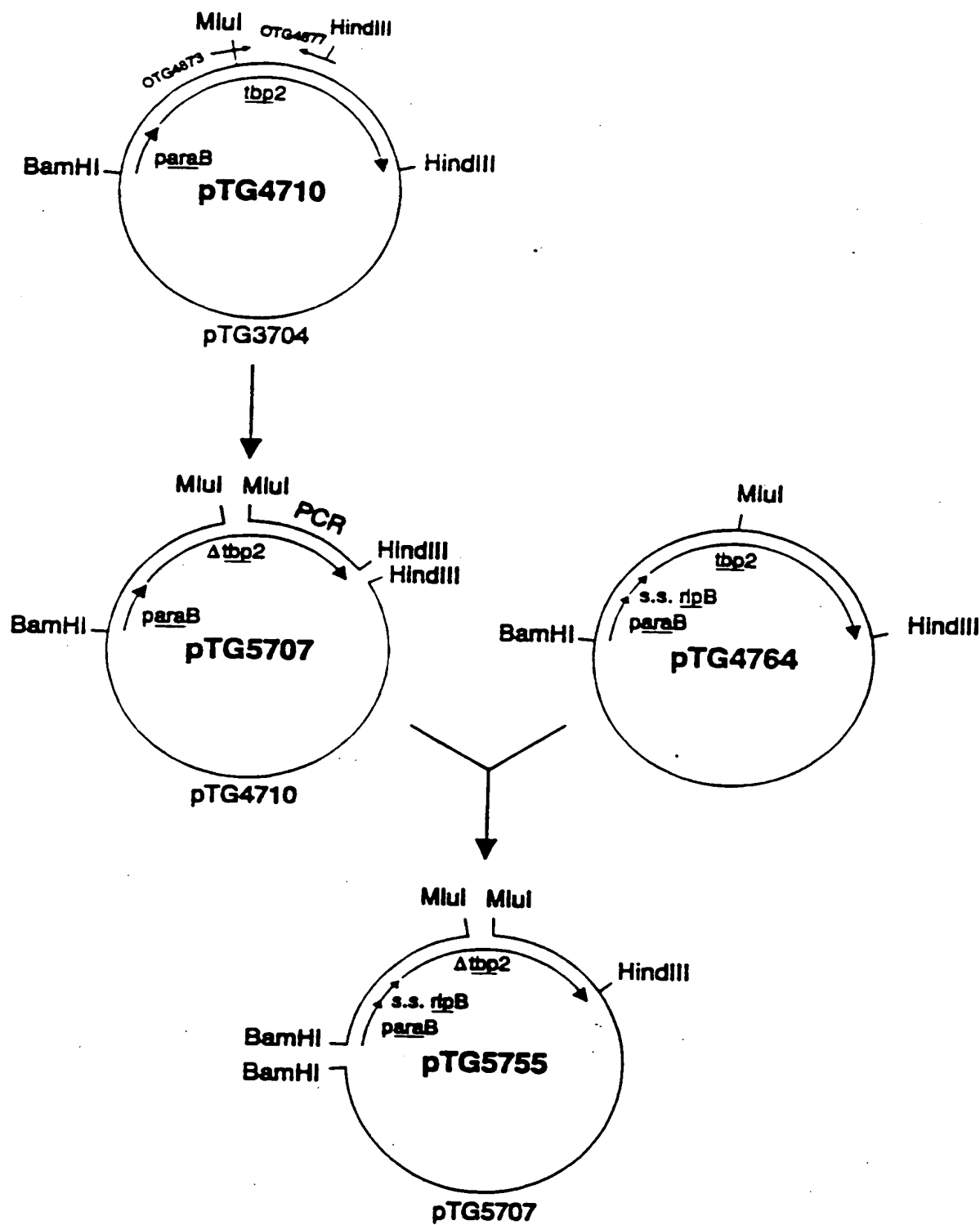
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Figure 5



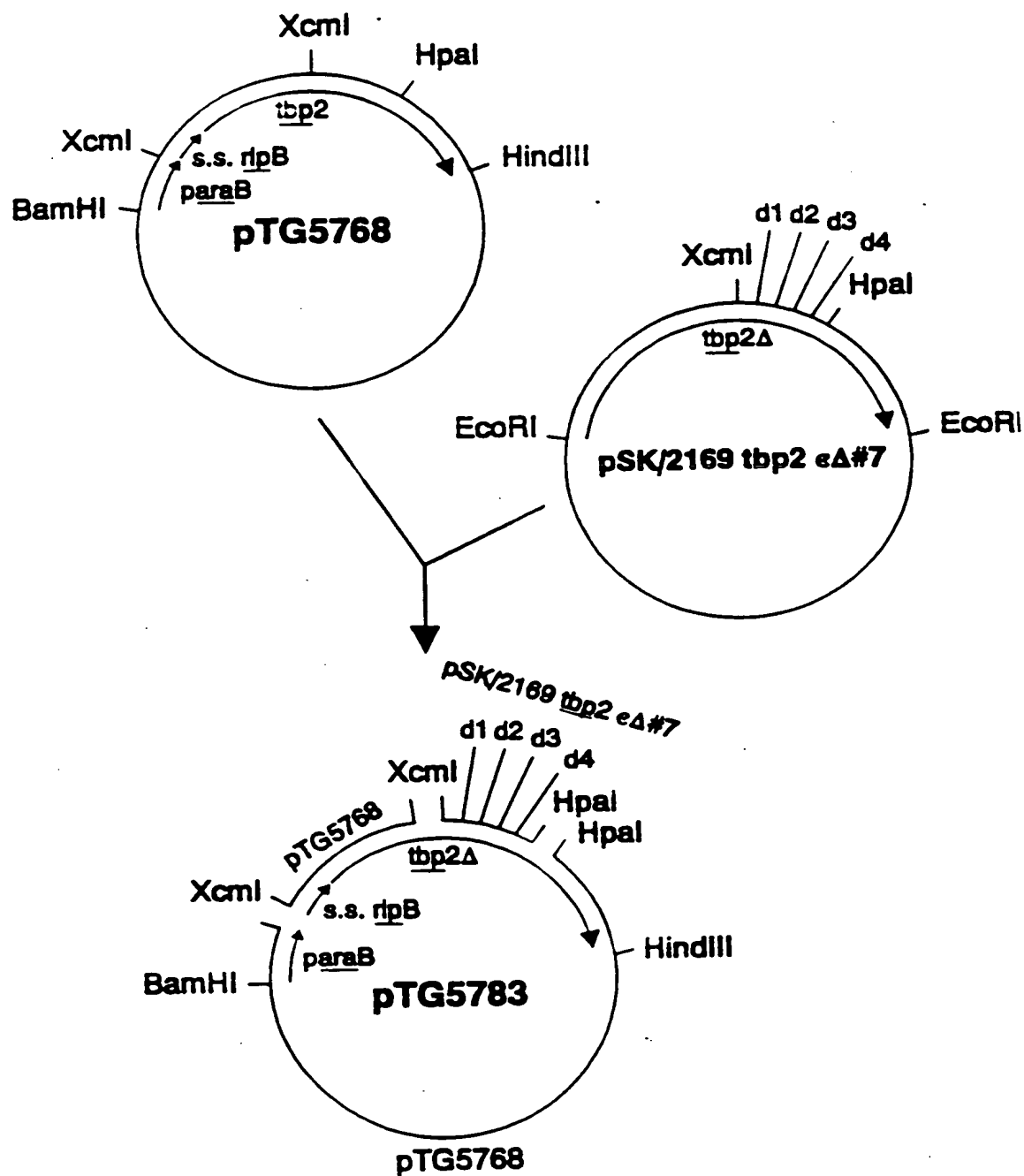
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Figure 6



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Figure 7



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Figure 8

M982

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BZ83

```
      10      20      30      40      50      60      70
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSSEKPAQAKDQGGYGFMRLKRRNWYPGAESEVKLNESDWEA
=====
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSSETPQAQKDQGGYGFMRFKRRNWYPKNEEDHKALSEADWEK
      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
TGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLTPSNHQNGSAGNGVNPKNQATGHENFQYVYSGWF
= - - - - - = - - - - - = - - - - - = - - - - - = - - - - - = - - - - - = - - - - -
LG AGKPDEFPORNE ILN M TDG  ILSES L   QL GE G G   KSRVEGYTDFQYVRSGYI
      80      90     100     110     120

      150     160     170     180     190     200     210
YKHAASEKDFSNNKKIKSGDDGYIFYHGEKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQPSKKQGD
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
YRNGANKIDFQKKIALSGPDGYLFYKGSNPSQALPM GKVGYKGTWDYVTDAKMGQKFSQL AGFPAGD
      130     140     150     160     170     180

      220     230     240     250     260     270     280
RYSGFSGDGSSEEYSNNKNESTLKDDHEGYGFTSNLEVDFGNKKLTGKLIRNNASLNNNTNNDKHTTQYYSL
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
RYGALSAAEEADVLRNKSEA  QQGQTDGFLTSEFEVDFAAKTMTGALYRNNRITNNETENKAKQIKRYDI
      200     210     220     230     240     250

      290     300     310     320     330     340
DAQITGNRNFNGTATATDK KENETKLHPFVSDSSSLSGGFFGPGQGEELGFRFLSDDQKVAVVGSAKTKDK
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
QADLHGNNRFGSKATATDKPKNDETKEHPFVSDSSSLSGGFFGPKGEELGFRFLSDDQKVAVVGSAKTKDK
      260     270     280     290     300     310     320

      360     370     380     390     400     410
LENGAAASGSTGAAASGGAAGTSSNSKLTTLVDAVELTLNDKKIKNLDNFSNAAQLVVDGIMIPLLPKD
=====
LENGAAASGSTGAAASGGAADMPSENGKLTTLVDAVELKSGGKEVKNLDNFSNAAQLVVDGIMIPLLPKN
      330     340     350     360     370     380     390

      430     440     450     460     470     480
SESGNTQADKGKNGGTEFTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCSNLNY
=====
SESESNQADKGKNGGTAFTTRKFEHTPESDKKDTQAGTAENGNNPAASNTAGDTNGKTKTYEVEVCCSNLNY
      400     410     420     430     440     450     460

      500     510     520     530     540     550
LKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLOGERTDEKEIPTDQ NVVYRGSWYGHIANGTSW
=====
LKYGMLTRKNSKSAMQAGENGSLADAKTEQVEQSMFLOGERTDEKEIPKEQQDIVYRGSWYGHIANDTSW
      470     480     490     500     510     520     530

      570     580     590     600     610     620
SGNASDKEGGNRAEFTVNFADKKITGKLTAEENRQAQFTTIEGMIQNGFEGTAKTAESGFDLDQKNTTTRT
=====
SGNASDREGGNRADFTVNFGTKKINGTLTAENRQEATFTIVGDIKDNGFEGTAKTADSGFDLDQSNTTTRT
      540     550     560     570     580     590     600
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	640	650	660	670	680	690
	PKAYITDAKVKGGFYGP	KAEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQOPVQ				
	=====					
	PKAYITDAKVKGGFYGP	KAEELGGWFAYPGDKQTEKATVTSGDGLSASSATVVFGAKRQKPVO				
610	620	630	640	650	660	

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Figure 9

M982

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BZ163

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      10      20      30      40      50      60
CLGGGGSFDLDSVDTEAPRPAP KYQDVSSSEKPPQAQKDQGGYGFMRLKRRNWYPGAESEVKLNESDWE
=====
CLGGGGSFDLDSVDTEAPRPAPPKYQDVSSSEKPPQAQKDQGGYGFMRLKRRNRHPQAKEDKVELNPNPNDWE
      10      20      30      40      50      60      70

      80      90     100     110     120     130
ATGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLTSPSNHQNGSAGNGVNOPKNQATGHENFQYVYSGW
=====
ETGLPSKPQNLPERQQSVIDKVKTDDGSNIYTSPLYTQSNHQNGSTNSGANQPKNEVKDYKNFKYVYSGW
      80      90     100     110     120     130     140

      150     160     170     180     190     200
FYKHAASEKDFSNKKIKSGDDGYIFYHGEKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQPSKKQG
=====
FYKHAESEREFSEKIKFKSGDDGYIFYHKGDPKPSRQLPTSEKVIYKGVWHFVTDTEKGQKFNDEILETSKGQG
      150     160     170     180     190     200     210

      220     230     240     250     260     270
DRYSGFSGDGSSEYSNKNESTLKDDHEGYGFTSNLEVDVFGNKKLTGKLI RNNASLNNNTNNDKHTTQYYS
=====
DRYSGFSGDDGETTSNRDTSNLDKHEGYGFTSNLEVDVFGSKKLTGKLI RNN RVTNATTNDKYTTQYYS
      220     230     240     250     260     270

      290     300     310     320     330     340
LDAQITGNRFNGTATATDKKENE TKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVGSAKTKD
=====
LDAQITGNRFNGKAIADKPDGTTGKLHPFVSDSSSLSGGFFGPKGEELGFRFLSDDKKVAVVGSAKTKD
      290     300     310     320     330     340

      360     370     380     390     400     410
KLENGAAASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIMIPLLPK
=====
KTENGAVASGGTDAAASNGAAGTSSSENSKLTTVLDAVELKLGDKEVQKLDNFSNAAQLVVDGIMIPLLPE
      360     370     380     390     400     410

      430     440     450     460     470     480
DSESGNTQADKGNKGGTEFTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCSNLN
=====
TSESGNNQANQGTNGGTAFTTRKFDHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCSNLN
      430     440     450     460     470     480

      500     510     520     530     540     550
YLKYGMLTRKNKSKSAMQAGGNSSQADAKTEQVEQSMFLOGERTDEKEIPTDQNVVYRGSWYGHIANGTSW
=====
YLKYGMLTRKNKSKSAMQAGESSSQADAKTEQVGQSMFLOGERTDEKEIPSEQNIVYRGSWYGHIASSTSW
      500     510     520     530     540     550

      570     580     590     600     610     620
SGNASDKEGGNRAEFTVNFADKKITGKLTAENRQAQFTTIEGMIQNGNGFEGTAKTAESGFDLDQKNTTTRT
=====
SGNASDKEGGNRAEFTVNFGEKKITGTLTAENRQEATFTIDGKIEGNGFSGTAKTAELGFDLDQKNTTTRT
      570     580     590     600     610     620
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640	650	660	670	680	690
PKAYITDAKVKGGFYGPKEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQOPVQ					
=====					
PKAYITDAKVQGGFYGPKEELGGWFAYQGDQKTENTTVASGNGNSASSATVVFGAKRQKPVQ					
640	650	660	670	680	690

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Figure 10

	10	20	30	40	50	60	
	346	361	380				
1	TKDKLENG--AAASGSTGAAASGGAAGTSSSENSKLT	TTVLDAVELT	LNDKKIKNLDNFSN				57
2	TKDKTENG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELKLGDKEVQKLDNFSN					57
3	TQDKPRNG--AVASGGTGAARSNGAAGQSSSENSKLT	TTVLDAVELT	LNDKKIKNLDNFSN				57
4	TKDNTANGNTAAASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELT	LNDKKIKNLDNFSN				60
5	TKDKTENG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELKLGDKEVQKLDNFSN					57
6	TQDKAANGNTAAASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELT	LNDKKIKNLDNFSN				59
7	RKDKAESGGGNGASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELKSGGKEVQKLDNFSN					59
8	TKDKPANGNTAEASGGTDAASGGAAGTSSSENSKLT	TTVLDAVELTHGGTAIKNLDNFSN					59
9	TKDKPRNG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELT	LNDKKIKNLDNFSN				57
10	TKDKLENG--AAASGSTGAAASGGAADMPSENGKLT	TTVLDAVELKSGGKEVQKLDNFSN					57
11	TKDKTENG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELKLGDKEVQKLDNFSN					57
C	**D...*G...:ASG*T+AA*S+GAA***SEN+KLTTVLDAVEL:++*::++LDNFSN						
	70	80	90	100	110	120	
	417				445		
1	AAQLVVDGIMIPLLPKDSESGNTQADKGGK-----	NGGTEFTRKFEHT	PESDKKDAQAGT				111
2	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFDHT	PESDKKDAQAGT				111
3	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFNET	PKSDEKDTQAGT				111
4	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFAHT	PKSDEKDTQAGT				114
5	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFDHT	PESDKKDAQAGT				111
6	AAQLVVDGIMIPLLPETSESGSNQADKGGKNGKNGG	TDFTYKTTYTPKNDDKDTKAQT					119
7	AAQLVVDGIMIPLLPKDSESGNTQADKGGK-----	NGGTFTRKFEHT	PESDKKDAQAGT				113
8	AAQLVVDGIMIPLLPQNSTGKNNQPDQGGK-----	NGGTAFIYKTTYTPKNDDKDTKAQT					113
9	AAQLVVDGIMIPIMPETSESGNNQADKGGK-----	NGGTAFTRKFDHT	PKSDEKDTQAGT				111
10	AAQLVVDGIMIPLLPKNSESESNQADKGGK-----	NGGTAFTRKFEHT	PESDKKDTQAGT				111
11	AAQLVVDGIMIPLLPETSESGNNQANQGT-----	NGGTAFTRKFDHT	PESDKKDAQAGT				111
C	AAQLVV*GIMIP*P+.S***+*Q*::G: NGGT+F**K*.*TP:*D:KD:+A*T						
	130	140	150	160	170	180	
	465		482		499		
1	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNS					166
2	QANGAQTASNTAGDTNG-----	KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESS					166
3	AENGNPAAASNTAGDANG-----	KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESS					166
4	AANGDQAASNTAGDTNG-----	KTKTYEVEVCCSNLNYLKYGLLTRKTAGNTGEGGNGSQ					169
5	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESS					166
6	GAAGSSGAQTDLGRADVNGGKAETKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNS						179
7	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNLNYLKYGLLTRKTAGNTGEGGNGSQ					168
8	VTGGTQTASNTAGDANG-----	KTKTYEVEVCCSNLNYLKYGLLTRKTAGNTVGSGNSP					168
9	PTNGAQTASGTAGVTGGQAG----	KTYAVEVCCSNLNYLKYGLLTRKTADNTVGSGNGSS					167
10	AENGNPAAASNTAGDTNG-----	KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGENG					166
11	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESS					166
C	:::G:++A***G***. :+KTY*VEVCCSNLNYLKYG+LTRK++++++G::**						

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Figure 10 (continuation)

	190	200	210	
	521			
1	QADAKTEQVEQSMFLOGERTDEKEIPTDQ-NVV			198
2	QADAKTEQVGQSMFLOGERTDEKEIPSEQ-NIV			198
3	QADAKTEQVGQSMFLOGERTDEKEIPNDQ-NVV			198
4	TAAAQTAQGAQSMFLOGERTDEKEIPSEQ-NV-			200
5	QADAKTEQVEQSMFLOGERTDEKEIPSEQ-NIV			198
6	QADAKTEQVEQSMFLOGERTDEKEIPNDQ-NV-			210
7	TAAAQTAQGAQSMFLOGERTDEKEIPSEQ-NV-			199
8	TAAAQT--DAQSMFLOGERTDENKIPSEQ-NVV			198
9	TAAAQTAQGAQSMFLOGERTDEKEIPKEQQDIV			200
10	LADAKTEQVEQSMFLOGERTDEKEIPKEQQDIV			199
11	QADAKTEQVGQSMFLOGERTDEKEIPSEQ-NIV			198
C	:A+A+T+++.QSMFLOGERTDE**IP:+Q *:+			